



1

SEQUENCE LISTING

<110> TAKASHIMA, SHOU
TSUJIMOTO, MASAFUMI
TSUJI, SHUICHI

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<141> 2004-07-29

<150> PCT/JP03/00883

<151> 2003-01-30

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<150> JP 2002-122673

<151> 2002-04-24

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<170> PatentIn Ver. 3.3

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 tcattctgcc acccatctgc attaagacac aaggtgctga ccgcagagac ctgcc atg 178
 Met
 1
 aaa cca cac ttg aag caa tgg aga caa cga atg ctt ttc gga ata ttc 226
 Lys Pro His Leu Lys Gln Trp Arg Gln Arg Met Leu Phe Gly Ile Phe
 5 10 15
 gct tgg ggg ctc ctc ttt ttg ctg att ttc atc tac ttc acc gac agc 274
 Ala Trp Gly Leu Leu Phe Leu Leu Ile Phe Ile Tyr Phe Thr Asp Ser
 20 25 30

aac ccc gct gag cct gta ccc agc tcc ctc tcc ttc ctg gag acc agg	322
Asn Pro Ala Glu Pro Val Pro Ser Ser Leu Ser Phe Leu Glu Thr Arg	
35 40 45	
agg ctc ctg ccg gtg cag ggg aag cag cgg gcc atc atg ggc gcc gca	370
Arg Leu Leu Pro Val Gln Gly Lys Gln Arg Ala Ile Met Gly Ala Ala	
50 55 60 65	
cat gag ccc tcc ccg cct ggg ggc ctg gac gca cgc cag gcg ctg ccc	418
His Glu Pro Ser Pro Pro Gly Gly Leu Asp Ala Arg Gln Ala Leu Pro	
70 75 80	
cgc gcc cac cca gcc ggt tcc ttt cat gcg ggg cct gga gac ctg cag	466
Arg Ala His Pro Ala Gly Ser Phe His Ala Gly Pro Gly Asp Leu Gln	
85 90 95	
aaa tgg gcc cag tcc caa gat ggg ttt gaa cat aaa gag ttt ttt tca	514
Lys Trp Ala Gln Ser Gln Asp Gly Phe Glu His Lys Glu Phe Phe Ser	
100 105 110	
tcc cag gtg ggg aga aaa tct caa agt gct ttc tac ccg gag gat gac	562
Ser Gln Val Gly Arg Lys Ser Gln Ser Ala Phe Tyr Pro Glu Asp Asp	
115 120 125	
gac tac ttt ttt gct gct ggt cag cca ggg tgg cac agc cac act cag	610
Asp Tyr Phe Phe Ala Ala Gly Gln Pro Gly Trp His Ser His Thr Gln	
130 135 140 145	
ggg aca ttg gga ttc cct tcc ccc ggg gag cca ggc cca cgg gag ggg	658
Gly Thr Leu Gly Phe Pro Ser Pro Gly Glu Pro Gly Pro Arg Glu Gly	
150 155 160	
gct ttt ccg gct gca cag gtc cag agg agg cgg gtg aag aag agg cac	706
Ala Phe Pro Ala Ala Gln Val Gln Arg Arg Arg Val Lys Lys Arg His	
165 170 175	
cgg agg cag aga agg agc cac gtg ttg gag gag ggc gac gac ggc gac	754
Arg Arg Gln Arg Arg Ser His Val Leu Glu Glu Gly Asp Asp Gly Asp	
180 185 190	
agg ctg tac tcc tcc atg tcc agg gcc ttc ctg tac cgg ctc tgg aag	802
Arg Leu Tyr Ser Ser Met Ser Arg Ala Phe Leu Tyr Arg Leu Trp Lys	
195 200 205	
ggg aac gtc tct tcc aaa atg ctg aac ccg cgc ctg cag aag gcg atg	850
Gly Asn Val Ser Ser Lys Met Leu Asn Pro Arg Leu Gln Lys Ala Met	
210 215 220 225	
aag gat tac ctg acc gcc aac aag cac ggg gtg cgc ttc cgc ggg aag	898
Lys Asp Tyr Leu Thr Ala Asn Lys His Gly Val Arg Phe Arg Gly Lys	
230 235 240	
cgg gag gcc ggg ctg agc agg gca cag ctg ctg tgc cag ctg cgg agc	946
Arg Glu Ala Gly Leu Ser Arg Ala Gln Leu Leu Cys Gln Leu Arg Ser	
245 250 255	

cgc gcg cgc gtg cgg acg ctg gac ggc acc gag gcg ccc ttt tct gcg	994
Arg Ala Arg Val Arg Thr Leu Asp Gly Thr Glu Ala Pro Phe Ser Ala	
260 265 270	
ctg ggc tgg cgg cgc ctg gtg ccc gcc gtg ccc ctg agc cag ctg cac	1042
Leu Gly Trp Arg Arg Leu Val Pro Ala Val Pro Leu Ser Gln Leu His	
275 280 285	
ccc cgc ggc ctg cgc agc tgc gct gtc gtc atg tct gca ggc gca atc	1090
Pro Arg Gly Leu Arg Ser Cys Ala Val Val Met Ser Ala Gly Ala Ile	
290 295 300 305	
ctc aac tct tcc ttg ggc gag gaa ata gat tct cat gat gcg gtt ttg	1138
Leu Asn Ser Ser Leu Gly Glu Glu Ile Asp Ser His Asp Ala Val Leu	
310 315 320	
aga ttt aac tct gct cct aca cgt ggt tat gag aaa gat gtt ggg aat	1186
Arg Phe Asn Ser Ala Pro Thr Arg Gly Tyr Glu Lys Asp Val Gly Asn	
325 330 335	
aaa acc acc ata cgc atc att aat tcg cag att ctg acc aac ccc agc	1234
Lys Thr Thr Ile Arg Ile Ile Asn Ser Gln Ile Leu Thr Asn Pro Ser	
340 345 350	
cat cac ttc att gac agt tca ctg tat aaa gac gtc att ttg gtg gcc	1282
His His Phe Ile Asp Ser Ser Leu Tyr Lys Asp Val Ile Leu Val Ala	
355 360 365	
tgg gac cct gcc cca tat tcc gca aat ctt aac ctg tgg tac aaa aaa	1330
Trp Asp Pro Ala Pro Tyr Ser Ala Asn Leu Asn Leu Trp Tyr Lys Lys	
370 375 380 385	
ccg gat tac aac ctg ttc act cca tat att cag cat cgt cag aga aac	1378
Pro Asp Tyr Asn Leu Phe Thr Pro Tyr Ile Gln His Arg Gln Arg Asn	
390 395 400	
cca aat cag cca ttt tac att ctt cat cct aaa ttt ata tgg cag ctc	1426
Pro Asn Gln Pro Phe Tyr Ile Leu His Pro Lys Phe Ile Trp Gln Leu	
405 410 415	
tgg gat att atc cag gag aac act aaa gag aag att caa cca aac cca	1474
Trp Asp Ile Ile Gln Glu Asn Thr Lys Glu Lys Ile Gln Pro Asn Pro	
420 425 430	
cca tct tct ggt ttc att gga atc ctc atc atg atg tcc atg tgc aga	1522
Pro Ser Ser Gly Phe Ile Gly Ile Leu Ile Met Met Ser Met Cys Arg	
435 440 445	
gag gtg cac gtg tat gaa tat atc cca tcc gtg cgg cag acg gag ctg	1570
Glu Val His Val Tyr Glu Tyr Ile Pro Ser Val Arg Gln Thr Glu Leu	
450 455 460 465	
tgc cac tac cac gag ctg tac tac gac gca gcc tgc acc ctc ggg gcg	1618
Cys His Tyr His Glu Leu Tyr Tyr Asp Ala Ala Cys Thr Leu Gly Ala	
470 475 480	

tac cac cca cta ctc tat gag aag ctc ctg gtg cag cgc ctg aac atg 1666
 Tyr His Pro Leu Leu Tyr Glu Lys Leu Leu Val Gln Arg Leu Asn Met
 485 490 495

ggc acg cag ggg gat ttg cat cgc aag ggc aag gtg gtt ctt cct ggc 1714
 Gly Thr Gln Gly Asp Leu His Arg Lys Gly Lys Val Val Leu Pro Gly
 500 505 510

ttc cag gcg gtg cac tgc cct gca cca agt cca gtc att cca cac tct 1762
 Phe Gln Ala Val His Cys Pro Ala Pro Ser Pro Val Ile Pro His Ser
 515 520 525

taaaaagggt ttcttgggaa tcaatgtgca atggtaca 1800

<210> 7
 <211> 524
 <212> PRT
 <213> Mus sp.

<400> 7
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 1 5 10 15
 Phe Val Trp Gly Leu Leu Phe Leu Ala Ile Phe Ile Tyr Phe Thr Asn
 20 25 30
 Ser Asn Pro Ala Ala Pro Met Pro Ser Ser Phe Ser Phe Leu Glu Ser
 35 40 45
 Arg Gly Leu Leu Pro Leu Gln Gly Lys Gln Arg Val Ile Met Gly Ala
 50 55 60
 Leu Gln Glu Pro Ser Leu Pro Arg Ser Leu Asp Ala Ser Lys Val Leu
 65 70 75 80
 Leu Asp Ser His Pro Glu Asn Pro Phe His Pro Trp Pro Gly Asp Pro
 85 90 95
 Gln Lys Trp Asp Gln Ala Pro Asn Gly Phe Asp Asn Gly Asp Glu Phe
 100 105 110
 Phe Thr Ser Gln Val Gly Arg Lys Ser Gln Ser Ala Phe Tyr Pro Glu
 115 120 125
 Glu Asp Ser Tyr Phe Phe Val Ala Asp Gln Pro Glu Leu Tyr His His
 130 135 140
 Arg Gln Gly Ala Leu Glu Leu Pro Ser Pro Gly Glu Thr Ser Trp Arg
 145 150 155 160
 Ser Gly Pro Val Gln Pro Lys Gln Lys Leu Leu His Pro Arg Arg Gly
 165 170 175
 Ser Leu Pro Glu Glu Ala Tyr Asp Ser Asp Met Leu Ser Ala Ser Met
 180 185 190

Ser	Arg	Ala	Phe	Leu	Tyr	Arg	Leu	Trp	Lys	Gly	Ala	Val	Ser	Ser	Lys
		195						200				205			
Met	Leu	Asn	Pro	Arg	Leu	Gln	Lys	Ala	Met	Arg	Tyr	Tyr	Met	Ser	Phe
	210					215					220				
Asn	Lys	His	Gly	Val	Arg	Phe	Arg	Arg	Arg	Gly	Arg	Arg	Glu	Ala	Thr
225					230					235					240
Arg	Thr	Gly	Pro	Glu	Leu	Leu	Cys	Glu	Met	Arg	Arg	Arg	Val	Arg	Val
				245					250					255	
Arg	Thr	Leu	Asp	Gly	Arg	Glu	Ala	Pro	Phe	Ser	Gly	Leu	Gly	Trp	Arg
			260					265					270		
Pro	Leu	Val	Pro	Gly	Val	Pro	Leu	Ser	Gln	Leu	His	Pro	Arg	Gly	Leu
		275					280					285			
Ser	Ser	Cys	Ala	Val	Val	Met	Ser	Ala	Gly	Ala	Ile	Leu	Asn	Ser	Ser
	290					295					300				
Leu	Gly	Glu	Glu	Ile	Asp	Ser	His	Asp	Ala	Val	Leu	Arg	Phe	Asn	Ser
305					310					315					320
Ala	Pro	Thr	Arg	Gly	Tyr	Glu	Lys	Asp	Val	Gly	Asn	Lys	Thr	Thr	Val
				325					330					335	
Arg	Ile	Ile	Asn	Ser	Gln	Ile	Leu	Ala	Asn	Pro	Ser	His	His	Phe	Ile
			340					345					350		
Asp	Ser	Ala	Leu	Tyr	Lys	Asp	Val	Ile	Leu	Val	Ala	Trp	Asp	Pro	Ala
		355					360					365			
Pro	Tyr	Ser	Ala	Asn	Leu	Asn	Leu	Trp	Tyr	Lys	Lys	Pro	Asp	Tyr	Asn
	370					375					380				
Leu	Phe	Thr	Pro	Tyr	Ile	Gln	His	Arg	Arg	Lys	Tyr	Pro	Thr	Gln	Pro
385					390					395					400
Phe	Tyr	Ile	Leu	His	Pro	Lys	Phe	Ile	Trp	Gln	Leu	Trp	Asp	Ile	Ile
				405					410					415	
Gln	Glu	Asn	Thr	Arg	Glu	Lys	Ile	Gln	Pro	Asn	Pro	Pro	Ser	Ser	Gly
			420					425					430		
Phe	Ile	Gly	Ile	Leu	Ile	Met	Met	Ser	Met	Cys	Lys	Glu	Val	His	Val
		435					440					445			
Tyr	Glu	Tyr	Ile	Pro	Ser	Val	Arg	Gln	Thr	Glu	Leu	Cys	His	Tyr	His
	450					455					460				
Glu	Leu	Tyr	Tyr	Asp	Ala	Ala	Cys	Thr	Leu	Gly	Ala	Tyr	His	Pro	Leu
465					470					475					480
Leu	Tyr	Glu	Lys	Leu	Leu	Val	Gln	Arg	Leu	Asn	Thr	Gly	Thr	Gln	Ala
				485					490					495	

Asp Leu His His Lys Gly Lys Val Val Leu Pro Gly Phe Gln Thr Leu
 500 505 510

Arg Cys Pro Val Thr Ser Pro Asn Asn Thr His Ser
 515 520

<210> 8
 <211> 1611
 <212> DNA
 <213> Mus sp.

<220>
 <221> CDS
 <222> (3)..(1574)

<400> 8
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 Met Lys Pro His Leu Lys Gln Trp Arg Gln Arg Met Leu Phe Gly
 1 5 10 15
 ata ttt gtt tgg ggg ctc ctc ttt ttg gca att ttc atc tac ttc acc 95
 Ile Phe Val Trp Gly Leu Leu Phe Leu Ala Ile Phe Ile Tyr Phe Thr
 20 25 30
 aac agc aat cct gcg gca cct atg ccc agc tcc ttt tcc ttc ctg gag 143
 Asn Ser Asn Pro Ala Ala Pro Met Pro Ser Ser Phe Ser Phe Leu Glu
 35 40 45
 agc cgt ggg ctc ctg cct cta cag ggc aag cag cgg gtc atc atg ggc 191
 Ser Arg Gly Leu Leu Pro Leu Gln Gly Lys Gln Arg Val Ile Met Gly
 50 55 60
 gct ttg cag gaa ccc tct ttg ccc aga agt ttg gat gca agc aaa gtg 239
 Ala Leu Gln Glu Pro Ser Leu Pro Arg Ser Leu Asp Ala Ser Lys Val
 65 70 75
 ctt ctg gac agc cac cct gag aac cct ttc cac cct tgg cct ggg gac 287
 Leu Leu Asp Ser His Pro Glu Asn Pro Phe His Pro Trp Pro Gly Asp
 80 85 90 95
 cca cag aaa tgg gat cag gcc cca aat ggc ttt gac aat ggg gat gag 335
 Pro Gln Lys Trp Asp Gln Ala Pro Asn Gly Phe Asp Asn Gly Asp Glu
 100 105 110
 ttt ttt aca tcc cag gtt ggg agg aaa tca caa agc gct ttc tat ccc 383
 Phe Phe Thr Ser Gln Val Gly Arg Lys Ser Gln Ser Ala Phe Tyr Pro
 115 120 125
 gag gaa gat agc tat ttt ttt gtt gcg gat cag cct gag ttg tac cac 431
 Glu Glu Asp Ser Tyr Phe Phe Val Ala Asp Gln Pro Glu Leu Tyr His
 130 135 140
 cac agg cag ggt gca ctg gag ctg cca tct cca ggg gag aca tca tgg 479
 His Arg Gln Gly Ala Leu Glu Leu Pro Ser Pro Gly Glu Thr Ser Trp
 145 150 155

cga tca gga cct gtt cag ccc aag cag aag ctg ctt cac cca agg cga	527
Arg Ser Gly Pro Val Gln Pro Lys Gln Lys Leu Leu His Pro Arg Arg	
160 165 170 175	
ggc agc ttg cct gag gaa gcc tat gac agc gac atg ctg tca gcc tcc	575
Gly Ser Leu Pro Glu Glu Ala Tyr Asp Ser Asp Met Leu Ser Ala Ser	
180 185 190	
atg tcg aga gcc ttc ctg tac cgg ctc tgg aag ggg gcc gtg tcc tct	623
Met Ser Arg Ala Phe Leu Tyr Arg Leu Trp Lys Gly Ala Val Ser Ser	
195 200 205	
aag atg ttg aac ccg cgc ctg cag aag gcc atg cgt tac tac atg tcc	671
Lys Met Leu Asn Pro Arg Leu Gln Lys Ala Met Arg Tyr Tyr Met Ser	
210 215 220	
ttc aac aag cat ggt gtg cgc ttc cgc agg cgg ggt cgg cgt gaa gct	719
Phe Asn Lys His Gly Val Arg Phe Arg Arg Arg Gly Arg Arg Glu Ala	
225 230 235	
aca cgt aca ggg ccg gag ctg ctg tgt gag atg cgc aga cgt gtg cgt	767
Thr Arg Thr Gly Pro Glu Leu Leu Cys Glu Met Arg Arg Arg Val Arg	
240 245 250 255	
gtg cgc acg ttg gac ggc aga gag ggc ccc ttc tcg ggg ctg ggc tgg	815
Val Arg Thr Leu Asp Gly Arg Glu Ala Pro Phe Ser Gly Leu Gly Trp	
260 265 270	
cgg cct ctg gta cca ggt gta cct ctg agc cag ttg cac ccg cgc ggt	863
Arg Pro Leu Val Pro Gly Val Pro Leu Ser Gln Leu His Pro Arg Gly	
275 280 285	
ctg agc agc tgc gca gtt gtc atg tct gcc ggt gcc atc ctg aac tcc	911
Leu Ser Ser Cys Ala Val Val Met Ser Ala Gly Ala Ile Leu Asn Ser	
290 295 300	
tcc ttg ggg gag gaa atc gat tct cat gat gca gtt ttg aga ttt aac	959
Ser Leu Gly Glu Glu Ile Asp Ser His Asp Ala Val Leu Arg Phe Asn	
305 310 315	
tct gcc cct acc cgt ggc tac gag aaa gat gtc gga aat aaa acc aca	1007
Ser Ala Pro Thr Arg Gly Tyr Glu Lys Asp Val Gly Asn Lys Thr Thr	
320 325 330 335	
gta cgc atc att aat tct cag att ctg gcc aac ccc agc cat cac ttc	1055
Val Arg Ile Ile Asn Ser Gln Ile Leu Ala Asn Pro Ser His His Phe	
340 345 350	
att gac agt gct tta tat aaa gat gtt atc ctg gta gcc tgg gat cct	1103
Ile Asp Ser Ala Leu Tyr Lys Asp Val Ile Leu Val Ala Trp Asp Pro	
355 360 365	
gct cct tat tct gcc aat ctt aac ctg tgg tat aag aag cca gat tac	1151
Ala Pro Tyr Ser Ala Asn Leu Asn Leu Trp Tyr Lys Lys Pro Asp Tyr	
370 375 380	

aac ctt ttc act cca tat atc cag cat cgc cgg aaa tac ccg act cag	1199
Asn Leu Phe Thr Pro Tyr Ile Gln His Arg Arg Lys Tyr Pro Thr Gln	
385 390 395	
cca ttt tac att ctt cac ccc aag ttc ata tgg cag ctt tgg gac att	1247
Pro Phe Tyr Ile Leu His Pro Lys Phe Ile Trp Gln Leu Trp Asp Ile	
400 405 410 415	
atc cag gag aat aca agg gag aag ata cag ccc aac cca cca tct tct	1295
Ile Gln Glu Asn Thr Arg Glu Lys Ile Gln Pro Asn Pro Pro Ser Ser	
420 425 430	
ggg ttt att gga atc ctc atc atg atg tcc atg tgt aaa gag gtg cac	1343
Gly Phe Ile Gly Ile Leu Ile Met Met Ser Met Cys Lys Glu Val His	
435 440 445	
gtg tat gag tac atc cca tct gtt cga cag aca gag ctt tgc cac tac	1391
Val Tyr Glu Tyr Ile Pro Ser Val Arg Gln Thr Glu Leu Cys His Tyr	
450 455 460	
cat gag ctg tac tac gac gca gcc tgc acc ttg ggg gcc tac cac cca	1439
His Glu Leu Tyr Tyr Asp Ala Ala Cys Thr Leu Gly Ala Tyr His Pro	
465 470 475	
ctg ctc tat gaa aag cta ctg gtg cag cgc ctt aac aca ggc acc cag	1487
Leu Leu Tyr Glu Lys Leu Leu Val Gln Arg Leu Asn Thr Gly Thr Gln	
480 485 490 495	
gca gac ttg cat cac aag ggc aag gta gtc ttg cca ggc ttc cag acc	1535
Ala Asp Leu His His Lys Gly Lys Val Val Leu Pro Gly Phe Gln Thr	
500 505 510	
ctt cgg tgt cca gta acc agc ccc aac aat aca cat tct taaaatggaa	1584
Leu Arg Cys Pro Val Thr Ser Pro Asn Asn Thr His Ser	
515 520	
ctcttgggaa ctgatgtgca ataaggt	1611

<210> 9

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 9

cttttctgga gaactaaagg

20

<210> 10

<211> 20

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 10
 aattgcagtt tgaggattcc 20

<210> 11
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 11
 tggctcagga tgagatcggg 20

<210> 12
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 12
 tactagcgct ccctgtgatt gg 22

<210> 13
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 13
 tgctctcgag ccagccgac gcgcctgccc 30

<210> 14
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 14
 tattctcgag ctaagaaacg ttaagccgtt 30

<210> 15
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 15
 caattgacat atctgaatga gaagtcgctc

30

<210> 16
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 16
 tactaacatc tcctgtggtt gg

22

<210> 17
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 17
 ccagtgtccc agccttttgt

20

<210> 18
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 18
 tgagtgggga agctttggtc

20

<210> 19
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 19

gacaatgggg atgagttttt tacatcccag

30

<210> 20

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 20

cgatttcctc cccaaggag gagttcagg

29

<210> 21

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 21

acgttggacg gcagagaggc gcccttctcg

30

<210> 22

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 22

accttattgc acatcagttc ccaagagttc

30

<210> 23

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 23
caatgaaacc acacttgaag caatggcgac 30

<210> 24
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 24
cgcaacaaaa aaatagctat cttcctcggg 30

<210> 25
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 25
tcactactt cacctcgagc aaccccgctg 30

<210> 26
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 26
catccaattg accaacagca atcctgcggc 30

<210> 27
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 27
ttatgattca caccaacctg aag 23

<210> 28
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 28
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23

<210> 29
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 29
 agacgtcatt ttggtggcct ggg

23

<210> 30
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 30
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21

<210> 31
 <211> 355
 <212> PRT
 <213> Mus sp.

<400> 31
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 1 5 10 15
 Met Leu Ala Arg Lys Phe Pro Arg Thr Arg Leu Pro Val Gly Ala Ser
 20 25 30
 Ala Leu Cys Val Val Val Leu Cys Trp Leu Tyr Ile Phe Pro Val Tyr
 35 40 45
 Arg Leu Pro Asn Glu Lys Glu Ile Val Gln Gly Val Leu Ala Gln Arg
 50 55 60

[illegible]

<210> 32
 <211> 412
 <212> PRT
 <213> Mus sp.

<400> 32

Met	Arg	Tyr	Ala	Asp	Pro	Ser	Ala	Asn	Arg	Asp	Leu	Leu	Gly	Asn	Arg	1	5	10	15
Thr	Leu	Leu	Phe	Ile	Phe	Ile	Cys	Ala	Phe	Ala	Leu	Val	Thr	Leu	Leu	20	25	30	
Gln	Gln	Ile	Leu	Tyr	Ser	Lys	Ser	Tyr	Ile	Lys	Arg	Gly	Phe	Gln	Phe	35	40	45	
Gly	Trp	Gln	Arg	Gly	Asp	Gln	Gln	Ala	Asn	Trp	Thr	Gly	Leu	Phe	Asn	50	55	60	
Asp	Ser	Asp	Ser	Pro	Thr	Glu	Gln	Asn	Ile	Thr	Gly	Ser	Ser	Ser	Arg	65	70	75	80
Tyr	Phe	Glu	Phe	Tyr	Lys	Glu	Pro	Leu	Glu	Phe	Asn	Ser	Thr	Arg	Cys	85	90	95	
Leu	Glu	Leu	Arg	Gln	Glu	Ile	Leu	Glu	Val	Lys	Val	Leu	Ser	Met	Val	100	105	110	
Lys	Gln	Ser	Glu	Leu	Phe	Glu	Arg	Trp	Lys	Ser	Leu	Gln	Ile	Cys	Lys	115	120	125	
Trp	Ala	Met	Gly	Ala	Ser	Glu	Ala	Ser	Leu	Phe	Lys	Ser	Thr	Leu	Ser	130	135	140	
Arg	Cys	Cys	Asn	Ala	Pro	Asn	Phe	Leu	Phe	Thr	Thr	Gln	Lys	Asn	Thr	145	150	155	160
Pro	Val	Glu	Thr	Asn	Leu	Arg	Tyr	Glu	Val	Glu	Ser	Ser	Gly	Leu	Tyr	165	170	175	
His	Ile	Asp	Gln	Glu	Ile	Phe	Lys	Met	Phe	Pro	Lys	Glu	Met	Pro	Tyr	180	185	190	
Tyr	Arg	Ser	Gln	Phe	Lys	Lys	Cys	Ala	Val	Val	Gly	Asn	Gly	Gly	Ile	195	200	205	
Leu	Lys	Asn	Ser	Gly	Cys	Gly	Lys	Glu	Ile	Asn	Ser	Ala	Asp	Phe	Val	210	215	220	
Phe	Arg	Cys	Asn	Leu	Pro	Pro	Ile	Ser	Gly	Ile	Tyr	Thr	Thr	Asp	Val	225	230	235	240
Gly	Glu	Lys	Thr	Asp	Val	Val	Thr	Val	Asn	Pro	Ser	Ile	Ile	Ile	Asp	245	250	255	
Arg	Phe	His	Lys	Leu	Glu	Lys	Trp	Arg	Arg	Pro	Phe	Phe	Ser	Val	Leu	260	265	270	

Gln Arg Tyr Glu Asn Ala Ser Val Leu Leu Pro Ala Phe Tyr Asn Val
 275 280 285
 Arg Asn Thr Leu Val Ser Phe Arg Val Lys Tyr Met Leu Asp Asp Phe
 290 295 300
 Gln Ser Arg Gln Pro Val Tyr Phe Phe His Pro Gln Tyr Leu Ser Ser
 305 310 315 320
 Val Ser Arg Tyr Trp Leu Ser Leu Gly Val Arg Ala Arg Arg Ile Ser
 325 330 335
 Thr Gly Leu Ser Leu Val Thr Ala Ala Leu Glu Leu Cys Glu Glu Val
 340 345 350
 His Leu Phe Gly Phe Trp Ala Phe Pro Met Asn Pro Ser Gly Phe Phe
 355 360 365
 Ile Thr His His Tyr Tyr Asp Asn Val Lys Pro Lys Pro Gly Phe His
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 Ala Met Pro Ser Glu Ile Phe Thr Phe Leu Arg Met His Ser Arg Gly
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 Ile Leu Arg Val His Thr Gly Thr Cys Asn Cys Cys
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 act aaa gag aag att caa cca aac cca cca tct tct ggt ttc att ggc 95
 Thr Lys Glu Lys Ile Gln Pro Asn Pro Pro Ser Ser Gly Phe Ile Gly
 20 25 30
 tca ttt gta aaa att ggc cat atc aga gct tgc agt gag ccg aga tca 143
 Ser Phe Val Lys Ile Gly His Ile Arg Ala Cys Ser Glu Pro Arg Ser
 35 40 45
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 Phe Leu Leu Phe Ala Val Ile Cys Val Trp Lys Glu Lys Lys Lys Gly
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 Ser Tyr Tyr Asp Ser Phe Lys Leu Gln Thr Lys Glu Phe Gln Val Leu
 35 40 45
 Lys Ser Leu Gly Lys Leu Ala Met Gly Ser Asp Ser Gln Ser Val Ser
 50 55 60
 Ser Ser Ser Thr Gln Asp Pro His Arg Gly Arg Gln Ala Leu Gly Ser
 65 70 75 80
 Leu Arg Asp Ile Pro Lys Ala Lys Pro Glu Ala Ser Phe Gln Val Trp
 85 90 95
 Asn Lys Asp Ser Ser Ser Lys Asn Leu Ile Pro Arg Leu Gln Lys Ile
 100 105 110
 Trp Lys Asn Tyr Leu Ser Met Asn Lys Tyr Lys Val Ser Tyr Lys Gly
 115 120 125
 Pro Gly Pro Gly Ile Lys Phe Ser Ala Glu Ala Leu Arg Cys His Leu
 130 135 140
 Arg Asp His Val Asn Val Ser Met Val Glu Val Thr Asp Phe Pro Phe
 145 150 155 160
 Asn Thr Ser Glu Trp Glu Gly Tyr Leu Pro Lys Glu Ser Ile Arg Thr
 165 170 175

Lys Ala Gly Pro Trp Gly Arg Cys Ala Val Val Ser Ser Ala Gly Ser
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 Leu Lys Ser Ser Gln Leu Gly Arg Glu Ile Asp Asp His Asp Ala Val
 195 200 205
 Leu Arg Phe Asn Gly Ala Pro Thr Ala Asn Phe Gln Gln Asp Val Gly
 210 215 220
 Thr Lys Thr Thr Ile Arg Leu Met Asn Ser Gln Leu Val Thr Thr Glu
 225 230 235 240
 Lys Arg Phe Leu Lys Asp Ser Leu Tyr Asn Glu Gly Ile Leu Ile Val
 245 250 255
 Trp Asp Pro Ser Val Tyr His Ser Asp Ile Pro Lys Trp Tyr Gln Asn
 260 265 270
 Pro Asp Tyr Asn Phe Phe Asn Asn Tyr Lys Thr Tyr Arg Lys Leu His
 275 280 285
 Pro Asn Gln Pro Phe Tyr Ile Leu Lys Pro Gln Met Pro Trp Glu Leu
 290 295 300
 Trp Asp Ile Leu Gln Glu Ile Ser Pro Glu Glu Ile Gln Pro Asn Pro
 305 310 315 320
 Pro Ser Ser Gly Met Leu Gly Ile Ile Ile Met Met Thr Leu Cys Asp
 325 330 335
 Gln Val Asp Ile Tyr Glu Phe Leu Pro Ser Lys Arg Lys Thr Asp Val
 340 345 350
 Cys Tyr Tyr Tyr Gln Lys Phe Phe Asp Ser Ala Cys Thr Met Gly Ala
 355 360 365
 Tyr His Pro Leu Leu Tyr Glu Lys Asn Leu Val Lys His Leu Asn Gln
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 385 390 395 400
 Phe Arg Thr Ile His Cys
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<213> Homo sapiens

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<222> (176)..(1762)

<400> 36

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 tcattctgcc acccatctgc attaagacac aaggtgctga ccgcagagac ctgcc atg 178
 Met
 1
 aaa cca cac ttg aag caa tgg aga caa cga atg ctt ttc gga ata ttc 226
 Lys Pro His Leu Lys Gln Trp Arg Gln Arg Met Leu Phe Gly Ile Phe
 5 10 15
 gct tgg ggg ctc ctc ttt ttg ctg att ttc atc tac ttc acc gac agc 274
 Ala Trp Gly Leu Leu Phe Leu Leu Ile Phe Ile Tyr Phe Thr Asp Ser
 20 25 30
 aac ccc gct gag cct gta ccc agc tcc ctc tcc ttc ctg gag acc agg 322
 Asn Pro Ala Glu Pro Val Pro Ser Ser Leu Ser Phe Leu Glu Thr Arg
 35 40 45
 agg ctc ctg ccg gtg cag ggg aag cag cgg gcc atc atg ggc gcc gca 370
 Arg Leu Leu Pro Val Gln Gly Lys Gln Arg Ala Ile Met Gly Ala Ala
 50 55 60 65
 cat gag ccc tcc ccg cct ggg ggc ctg gac gca cgc cag gcg ctg ccc 418
 His Glu Pro Ser Pro Pro Gly Gly Leu Asp Ala Arg Gln Ala Leu Pro
 70 75 80
 cgc gcc cac cca gcc ggt tcc ttt cat gcg ggg cct gga gac ctg cag 466
 Arg Ala His Pro Ala Gly Ser Phe His Ala Gly Pro Gly Asp Leu Gln
 85 90 95
 aaa tgg gcc cag tcc caa gat ggg ttt gaa cat aaa gag ttt ttt tca 514
 Lys Trp Ala Gln Ser Gln Asp Gly Phe Glu His Lys Glu Phe Phe Ser
 100 105 110
 tcc cag gtg ggg aga aaa tct caa agt gct ttc tac ccg gag gat gac 562
 Ser Gln Val Gly Arg Lys Ser Gln Ser Ala Phe Tyr Pro Glu Asp Asp
 115 120 125
 gac tac ttt ttt gct gct ggt cag cca ggg tgg cac agc cac act cag 610
 Asp Tyr Phe Phe Ala Ala Gly Gln Pro Gly Trp His Ser His Thr Gln
 130 135 140 145
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 Gly Thr Leu Gly Phe Pro Ser Pro Gly Glu Pro Gly Pro Arg Glu Gly
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 gct ttt ccg gct gca cag gtc cag agg agg cgg gtg aag aag agg cac 706
 Ala Phe Pro Ala Ala Gln Val Gln Arg Arg Arg Val Lys Lys Arg His
 165 170 175
 cgg agg cag aga agg agc cac gtg ttg gag gag ggc gac gac ggc gac 754
 Arg Arg Gln Arg Arg Ser His Val Leu Glu Glu Gly Asp Asp Gly Asp
 180 185 190
 agg ctg tac tcc tcc atg tcc agg gcc ttc ctg tac cgg ctc tgg aag 802
 Arg Leu Tyr Ser Ser Met Ser Arg Ala Phe Leu Tyr Arg Leu Trp Lys
 195 200 205

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Gly Asn Val Ser Ser Lys Met Leu Asn Pro Arg Leu Gln Lys Ala Met	
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aag gat tac ctg acc gcc aac aag cac ggg gtg cgc ttc cgc ggg aag	898
Lys Asp Tyr Leu Thr Ala Asn Lys His Gly Val Arg Phe Arg Gly Lys	
230 235 240	
cgg gag gcc ggg ctg agc agg gca cag ctg ctg tgc cag ctg cgg agc	946
Arg Glu Ala Gly Leu Ser Arg Ala Gln Leu Leu Cys Gln Leu Arg Ser	
245 250 255	
cgc gcg cgc gtg cgg acg ctg gac ggc acc gag gcg ccc ttt tct gcg	994
Arg Ala Arg Val Arg Thr Leu Asp Gly Thr Glu Ala Pro Phe Ser Ala	
260 265 270	
ctg ggc tgg cgg cgc ctg gtg ccc gcc gtg ccc ctg agc cag ctg cac	1042
Leu Gly Trp Arg Arg Leu Val Pro Ala Val Pro Leu Ser Gln Leu His	
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Pro Arg Gly Leu Arg Ser Cys Ala Val Val Met Ser Ala Gly Ala Ile	
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Leu Asn Ser Ser Leu Gly Glu Glu Ile Asp Ser His Asp Ala Val Leu	
310 315 320	
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Arg Phe Asn Ser Ala Pro Thr Arg Gly Tyr Glu Lys Asp Val Gly Asn	
325 330 335	
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Lys Thr Thr Ile Arg Ile Ile Asn Ser Gln Ile Leu Thr Asn Pro Ser	
340 345 350	
cat cac ttc att gac agt tca ctg tat aaa gac gtc att ttg gtg gcc	1282
His His Phe Ile Asp Ser Ser Leu Tyr Lys Asp Val Ile Leu Val Ala	
355 360 365	
tgg gac cct gcc cca tat tcc gca aat ctt aac ctg tgg tac aaa aaa	1330
Trp Asp Pro Ala Pro Tyr Ser Ala Asn Leu Asn Leu Trp Tyr Lys Lys	
370 375 380 385	
ccg gat tac aac ctg ttc act cca tat att cag cat cgt cag aga aac	1378
Pro Asp Tyr Asn Leu Phe Thr Pro Tyr Ile Gln His Arg Gln Arg Asn	
390 395 400	
cca aat cag cca ttt tac att ctt cat cct aaa ttt ata tgg cag ctc	1426
Pro Asn Gln Pro Phe Tyr Ile Leu His Pro Lys Phe Ile Trp Gln Leu	
405 410 415	
tgg gat att atc cag gag aac act aaa gag aag att caa cca aac cca	1474
Trp Asp Ile Ile Gln Glu Asn Thr Lys Glu Lys Ile Gln Pro Asn Pro	
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cca tct tct ggt ttc att gga atc ctc atc atg atg tcc atg tgc aga	1522
Pro Ser Ser Gly Phe Ile Gly Ile Leu Ile Met Met Ser Met Cys Arg	
435 440 445	
gag gtg cac gtg tat gaa tat atc cca tcc gtg cgg cag acg gag ctg	1570
Glu Val His Val Tyr Glu Tyr Ile Pro Ser Val Arg Gln Thr Glu Leu	
450 455 460 465	
tgc cac tac cac gag ctg tac tac gac gca gcc tgc acc ctc ggg gcg	1618
Cys His Tyr His Glu Leu Tyr Tyr Asp Ala Ala Cys Thr Leu Gly Ala	
470 475 480	
tac cac cca cta ctc tat gag aag ctc ctg gtg cag cgc ctg aac atg	1666
Tyr His Pro Leu Leu Tyr Glu Lys Leu Leu Val Gln Arg Leu Asn Met	
485 490 495	
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Gly Thr Gln Gly Asp Leu His Arg Lys Gly Lys Val Val Leu Pro Gly	
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ttc cag gcg gtg cac tgc cct gca cca agt cca gtc att cca cac tct	1762
Phe Gln Ala Val His Cys Pro Ala Pro Ser Pro Val Ile Pro His Ser	
515 520 525	
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